```
Qy    320 LLMHLGRYIPFLPSEKLERTSSV-SPSTAEPELSI 353


RESULT    7
ENTRY             A43113     #type complete
TITLE             chemokine (C-C) receptor 5 - human
ALTERNATE_NAMES   C-C CKR-5
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change
                    10-Sep-1997
ACCESSIONS        A43113
REFERENCE         A43113
   #authors       Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.;
                    Parmentier, M.
   #journal       Biochemistry (1996) 35:3362-3367
   #title         Molecular cloning and functional expression of a new human
                    CC-chemokine receptor gene.
   #accession     A43113
      ##status        preliminary
      ##molecule_type mRNA
      ##residues      1-352 ##label SAM
      ##cross-references GB:X91492; NID:g1262810; PID:e199247; PID:g1262811
SUMMARY           #length 352  #molecular-weight 40524  #checksum 6685

  Query Match           54.1%;  Score 1496;  DB 2;  Length 352;
  Best Local Similarity  54.3%;  Pred. No. 1.11e-195;
  Matches   182;  Conservative   88;  Mismatches  56;  Indels   9;  Gaps   9;

Db     20 CQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYLLNLAISDLFF 79
Qy     24 CEKADTRALMAQFVPPLYSLVFTFGLLGNVVVVMILIKYRRLRIMTNIYLLNLAISDLLF 83

Db     80 LLTVPFWAHYAAAQ-WDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVHAVFALK 138
Qy     84 LVTLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALR 143

Db    139 ARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYT-CSSHFPYSQ-YQFWKNFQTL 196
Qy    144 ARTVTFGVITSIVTWGLAVLAALPEFIFYETE-ELFEETLCSALYPEDTVYS-WRHFHTL 201

Db    197 KIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLL 256
Qy    202 RMTIFCLVLPLLVMAICYTGIIKTLLRCPS-KKKYKAIRLIFVIMAVFFIFWTPYNVAIL 260

Db    257 LNTFQEF-FGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKH 315
Qy    261 LSSYQSILFG-NDCERTKHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKYLRHFFHRH 319

Db    316 IAKRFCKCCSIFQQEAPERASSVYTRSTGEQEISV 350
Qy    320 LLMHLGRYIPFLPSEKLERTSSV-SPSTAEPELSI 353


RESULT    8
ENTRY             S55594     #type complete
TITLE             G protein-coupled receptor E1 - equine herpesvirus 2
ORGANISM          #formal_name equine herpesvirus 2
DATE              10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change
                    09-Sep-1997
ACCESSIONS        S55594
REFERENCE         S55594
   #authors       Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.;
                    Davison, A.J.
   #journal       J. Mol. Biol. (1995) 249:520-528
   #title         The DNA sequence of equine herpesvirus 2.
   #accession     S55594
      ##status        preliminary; nucleic acid sequence not shown
      ##molecule_type DNA
      ##residues      1-383 ##label TEL
      ##cross-references GB:U20824; NID:g695172; PID:g695173
KEYWORDS          G protein-coupled receptor
SUMMARY           #length 383  #molecular-weight 43667  #checksum 1663

  Query Match           52.5%;  Score 1452;  DB 2;  Length 383;
  Best Local Similarity  54.2%;  Pred. No. 4.19e-189;
  Matches   173;  Conservative   70;  Mismatches  74;  Indels   2;  Gaps   2;

Db     56 YEESAP-CYKSDTTRLAAQVVPALYLLVFLFGLLGNILVVIIVIRYMKIKNLTNMLLLNL 114
Qy     17 YDDVGLLCEKADTRALMAQFVPPLYSLVFTFGLLGNVVVVMILIKYRRLRIMTNIYLLNL 76

Db    115 AISDLLFLLTLPFWMHYIGMYHDWTFGISLCKLLRGVCYMSLYSQVFCIILLTVDRYLAV 174
Qy     77 AISDLLFLVTLPFWIHYV-RGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAI 135

Db    175 VYAVTALRFRTVTCGIVTCVCTWFLAGLLSLPEFFFHGHQDDNGRVQCDPYYPEMSTNVW 234
Qy    136 VHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALYPEDTVYSW 195

Db    235 RRAHVAKVIMLSLILPLLIMAVCYYVIIRRLLRRPSKKKYKAIRLIFVIMVAYFVFWTPY 294
Qy    196 RHFHTLRMTIFCLVLPLLVMAICYTGIIKTLLRCPSKKKYKAIRLIFVIMAVFFIFWTPY 255

Db    295 NIVLLLSTFHATLLNLQCALSSNLDMALLITKTVAYTHCCINPVIYAFVGEKFRRHLYHF 354
Qy    256 NVAILLSSYQSILFGNDCERTKHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKYLRHF 315

Db    355 FHTYVAIYLCKYIPFLSGD 373
Qy    316 FHRHLLMHLGRYIPFLPSE 334
```

SEQUENCE COMPARISON 'A'

```
RESULT    9
ENTRY             JC2443     #type complete
TITLE             chemokine (C-C) receptor 2, splice form B - human
ALTERNATE_NAMES   C-C CKR-2; monocyte chemoattractant protein 1 receptor;
                    monocyte chemotactin 1 receptor
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change
                    10-Sep-1997
ACCESSIONS        JC2443; I38463
REFERENCE         JC2443
   #authors       Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
   #journal       Biochem. Biophys. Res. Commun. (1994) 202:1156-1162
   #title         cDNA cloning and functional expression of a human monocyte
                    chemoattractant protein 1 receptor.
   #accession     JC2443
      ##molecule_type mRNA
      ##residues      1-360 ##label YAM
      ##cross-references DDBJ:D29984; NID:g531246; PID:d1006817; PID:g531247
REFERENCE         A53477
   #autnors       Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly,
                    A.J.; Coughlin, S.R.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756
   #title         Molecular cloning and functional expression of two monocyte
                    chemoattractant protein 1 receptors reveals alternate
                    splicing of the carboxyl-terminal tails.
   #cross-references MUID:94195821
   #accession     I38463
      ##status        preliminary
      ##molecule_type mRNA
      ##residues      1-360 ##label RES
      ##cross-references EMBL:U03905; NID:g472557; PID:g472558
GENETICS
   #gene          GDB:CMKBR2
      ##cross-references GDB:337364; OMIM:601267
   #map_position 3p21-3p21
KEYWORDS          alternative splicing; G protein-coupled receptor;
                    glycoprotein; transmembrane protein
FEATURE
   43-70              #domain transmembrane #status predicted #label TM1\
   81-100             #domain transmembrane #status predicted #label TM2\
   115-136            #domain transmembrane #status predicted #label TM3\
   154-178            #domain transmembrane #status predicted #label TM4\
   207-226            #domain transmembrane #status predicted #label TM5\
   244-268            #domain transmembrane #status predicted #label TM6\
```

```
  287-309          #domain transmembrane #status predicted #label TM7\
  14               #binding_site carbohydrate (Asn) (covalent) #status
                     predicted\
  113-190          #disulfide_bonds #status predicted
SUMMARY          #length 360  #molecular-weight 41063  #checksum 1732

  Query Match           52.0%;  Score 1438;  DB 2;  Length 360;
  Best Local Similarity 53.4%;  Pred. No. 5.17e-187;
  Matches  183;  Conservative   87;  Mismatches  63;  Indels  10;  Gaps   8;

Db      21 TTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIY 80
           |:::| | |  | | | : : ||::|||||||| ||::||::||:||: ::|: :|:||
Qy      14 TSYYD-DVGLLCEKADTRALMAQFVPPLYSLVFTFGLLGNVVVVMILIKYRRLRIMTNIY 72

Db      81 LLNLAISDLLFLITLPLWAHSA-ANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRY 139
           ||||||||||||:|||:| |   :::||||::||||::|:|| | :: ||||||||||||
Qy      73 LLNLAISDLLFLVTLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRY 132

Db     140 LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP--R- 196
           ||||||||||:|||||||:||:::|| :||:|::| :||   :       :|:: :|
Qy     133 LAIVHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALYPEDTV 192

Db     197 -GWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLF 255
            :| :|||:   |: |||||:| |||:||:|||||| : ||: :|:|:|| || |:|:|
Qy     193 YSWRHFHTLRMTIFCLVLPLLVMAICYTGIIKTLLRCPS-KKKYKAIRLIFVIMAVFFIF 251

Db     256 WTPYNIVILLNTFQEF-FGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRR 314
           |||||: |||:::| : || ::|| | :||    ||| :: :|||:||:|||||||:||:
Qy     252 WTPYNVAILLSSYQSILFG-NDCERTKHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRK 310

Db     315 YLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVS 357
           ||  ||:::|: ::: :  | :  | ::  ||: :|||:| |:|
Qy     311 YLRHFFHRHLLMHLGRYIPFLPSEKLE-RTSSVSPSTAEPELS 352


RESULT   10
ENTRY            I49340     #type complete
TITLE            MIP-1 alpha receptor like-1 - mouse
ORGANISM         #formal_name Mus musculus #common_name house mouse
DATE             02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                   28-Feb-1997
ACCESSIONS       I49340
REFERENCE        I49339
   #authors      Gao, J.L.; Murphy, P.M.
   #journal      J. Biol. Chem. (1995) 270:17494-17501
   #title        Cloning and differential tissue-specific expression of three
                   mouse beta chemokine receptor-like genes, including the
                   gene for a functional macrophage inflammatory protein-1
                   alpha receptor.
   #cross-references MUID:95340546
   #accession    I49340
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues      1-356 ##label RES
      ##cross-references EMBL:U28405; NID:g881549; PID:g881550
SUMMARY          #length 356  #molecular-weight 40934  #checksum 563

  Query Match           51.8%;  Score 1433;  DB 2;  Length 356;
  Best Local Similarity 52.0%;  Pred. No. 2.88e-186;
  Matches  173;  Conservative   78;  Mismatches  80;  Indels   2;  Gaps   2;

Db      22 GFLCFSINVRAFGITVPTPLYSLVFIIGVIGHVLVVLVLIQHKRLRNMTSIYLFNLAISD 81
           |:||   : ||:      ||||||| :|:::|:|:||::||  :||| ||:|||:||||||
Qy      21 GLLCEKADTRALMAQFVPPLYSLVFTFGLLGNVVVVMILIKYRRLRIMTNIYLLNLAISD 80

Db      82 LVFLSTLPFWVDYIMKGDWIFGNAMCKFVSGFYYLGLYSDMFFITLLTIDRYLAVVHVVF 141
           |:|| |||||: |:   :|:||::|||::|||| ||||::||| ||||||||:|| ||
Qy      81 LLFLVTLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVF 140

Db     142 ALRARTVTFGIISSIITWVLAALVSIPCLYVF-KSQMEFTYHTCRAILPRKSLIRFLRFQ 200
           ||||||||||:|:||:|| || | ::|  ::|  ::  |    | |: |  ::    :|:
Qy     141 ALRARTVTFGVITSIVTWGLAVLAALP-EFIFYETEELFEETLCSALYPEDTVYSWRHFH 199

Db     201 ALTMNILGLILPLLAMIICYTRIINVLHRRPNKKKAKVMRLIFVITLLFFLLLAPYYLAA 260
           :| | |: |:|||| | |||| ||: | | |:||| | :||||||  :||:: :|| :|
Qy     200 TLRMTIFCLVLPLLVMAICYTGIIKTLLRCPSKKKYKAIRLIFVIMAVFFIFWTPYNVAI 259

Db     261 FVSAFEDVLFTPSCLRSQQVDLSLMITEALAYTHCCVNPVIYVFVGKRFRKYLWQLFRRH 320
           ::|::: :||   | |: ::|| :::|| :||:|||:|||||| ||| ||||||:::|:||
Qy     260 LLSSYQSILFGNDCERTKHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKYLRHFFHRH 319

Db     321 TAITLPQWLPFLSEDRAQRASARLPSTVEIETS 353
           : | : :|||: :: :|:|:  ||| | | |
Qy     320 LLMHLGRYIPFLPSEKLERTSSVSPSTAEPELS 352


RESULT   11
ENTRY            I38450     #type complete
TITLE            chemokine (C-C) receptor 2, splice form A - human
ALTERNATE_NAMES  C-C CKR-2; monocyte chemoattractant protein 1 receptor;
                   monocyte chemotactin 1 receptor
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change
                   29-Aug-1997
ACCESSIONS       I38450
REFERENCE        A53477
   #authors      Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly,
                   A.J.; Coughlin, S.R.
   #journal      Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756
   #title        Molecular cloning and functional expression of two monocyte
                   chemoattractant protein 1 receptors reveals alternate
                   splicing of the carboxyl-terminal tails.
   #cross-references MUID:94195821
   #accession    I38450
      ##status        preliminary
      ##molecule_type mRNA
      ##residues      1-374 ##label RES
      ##cross-references EMBL:U03882; NID:g472555; PID:g472556
GENETICS
   #gene         GDB:CMKBR2
      ##cross-references GDB:337364; OMIM:601267
   #map_position 3p21-3p21
KEYWORDS         alternative splicing; G protein-coupled receptor;
                   glycoprotein; transmembrane protein
FEATURE
   44-68             #domain transmembrane #status predicted #label TM1\
   79-99             #domain transmembrane #status predicted #label TM2\
   115-136           #domain transmembrane #status predicted #label TM3\
   154-178           #domain transmembrane #status predicted #label TM4\
   208-226           #domain transmembrane #status predicted #label TM5\
   244-265           #domain transmembrane #status predicted #label TM6\
   292-309           #domain transmembrane #status predicted #label TM7\
   14                #binding_site carbohydrate (Asn) (covalent) #status
                       predicted\
   32-277,113-190    #disulfide_bonds #status predicted
SUMMARY          #length 374  #molecular-weight 41914  #checksum 5414

  Query Match           48.9%;  Score 1352;  DB 2;  Length 374;
  Best Local Similarity 56.2%;  Pred. No. 3.51e-174;
  Matches  168;  Conservative   72;  Mismatches  50;  Indels   9;  Gaps   7;

Db      21 TTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIY 80
           |:::| | |  | | | : : ||::|||||||| ||::||::||:||: ::|: :|:||
Qy      14 TSYYD-DVGLLCEKADTRALMAQFVPPLYSLVFTFGLLGNVVVVMILIKYRRLRIMTNIY 72

Db      81 LLNLAISDLLFLITLPLWAHSA-ANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRY 139
           ||||||||||||:|||:| |   :::||||::||||::|:|| | :: ||||||||||||
Qy      73 LLNLAISDLLFLVTLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRY 132

Db     140 LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP--R- 196
           ||||||||||:|||||||:||:::|| :||:|::| :||   :       :|:: :|
Qy     133 LAIVHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALYPEDTV 192

Db     197 -GWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLF 255
            :| :|||:   |: |||||:| |||:||:|||||| : ||: :|:|:|| || |:|:|
Qy     193 YSWRHFHTLRMTIFCLVLPLLVMAICYTGIIKTLLRCPS-KKKYKAIRLIFVIMAVFFIF 251
```